## SEQUENCE LISTING

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     Ruben, Steven
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  Ala Arg Val Asp Thr Asp Glu Asp Arg Tyr Pro Gln Lys Leu Ala Phe
                                                                        97
 gcc gag tgc ctg tgc aga ggc tgt atc gat gca cgg acg ggc cgc gag
 Ala Glu Cys Leu Cys Arg Gly Cys Ile Asp Ala Arg Thr Gly Arg Glu
 aca gct gcg ctc aac tcc gtg cgg ctg ctc cag agc ctg ctg gtg ctg
                                                                       145
 Thr Ala Ala Leu Asn Ser Val Arg Leu Leu Gln Ser Leu Leu Val Leu
 cgc cgc cgg ccc tgc tcc cgc gac ggc tcg ggg ctc ccc aca cct ggg
                                                                       193
 Arg Arg Pro Cys Ser Arg Asp Gly Ser Gly Leu Pro Thr Pro Gly
                         55
 gcc ttt gcc ttc cac acc gag ttc atc cac gtc ccc gtc ggc tgc acc
                                                                       241
 Ala Phe Ala Phe His Thr Glu Phe Ile His Val Pro Val Gly Cys Thr
                     70
 tgc gtg ctg ccc cgt tca gtg tgaccgccaa ggccgtgggg cccttagact
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 Cys Val Leu Pro Arg Ser Val
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<212> PRT

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Ala Glu Cys Leu Cys Arg Gly Cys Ile Asp Ala Arg Thr Gly Arg Glu 20 25 30

Thr Ala Ala Leu Asn Ser Val Arg Leu Leu Gln Ser Leu Leu Val Leu 35 40 45

Arg Arg Arg Pro Cys Ser Arg Asp Gly Ser Gly Leu Pro Thr Pro Gly 50 55 60

Ala Phe Ala Phe His Thr Glu Phe Ile His Val Pro Val Gly Cys Thr 65 70 75 80

Cys Val Leu Pro Arg Ser Val

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	143
agc gtg tcg ccc tgg gcc tac aga atc tcc tac gac ccg gcg agg tac Ser Val Ser Pro Trp Ala Tyr Arg Ile Ser Tyr Asp Pro Ala Arg Tyr 50 55 60	191
ccc agg tac ctg cct gaa gcc tac tgc ctg tgc cgg ggc tgc ctg acc Pro Arg Tyr Leu Pro Glu Ala Tyr Cys Leu Cys Arg Gly Cys Leu Thr 65 70 75	239
ggg ctg ttc ggc gag gag gac gtg cgc ttc cgc agc gcc cct gtc tac Gly Leu Phe Gly Glu Glu Asp Val Arg Phe Arg Ser Ala Pro Val Tyr 80 85 90 95	287
atg ccc acc gtc gtc ctg cgc cgc acc ccc gcc tgc gcc ggc ggc cgt Met Pro Thr Val Val Leu Arg Arg Thr Pro Ala Cys Ala Gly Gly Arg 100 105 110	335
tcc gtc tac acc gag gcc tac gtc acc atc ccc gtg ggc tgc acc tgc Ser Val Tyr Thr Glu Ala Tyr Val Thr Ile Pro Val Gly Cys Thr Cys 115 120 125	383
gtc ccc gag ccg gag aag gac gca gac agc atc aac tcc agc atc gac Val Pro Glu Pro Glu Lys Asp Ala Asp Ser Ile Asn Ser Ser Ile Asp 130 135 140	431
aaa cag ggc gcc aag ctc ctg ctg ggc ccc aac gac gcg ccc gct ggc Lys Gln Gly Ala Lys Leu Leu Leu Gly Pro Asn Asp Ala Pro Ala Gly 145 150 155	479
ccc tgaggccggt cctgccccgg gaggtctccc cggcccgcat cccgaggcgc Pro 160	532
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Gly Arg Pro Ala Asp Arg Arg Phe Arg Pro Pro Thr Asn Leu Arg Ser

Val Ser Pro Trp Ala Tyr Arg Ile Ser Tyr Asp Pro Ala Arg Tyr Pro 55

Arg Tyr Leu Pro Glu Ala Tyr Cys Leu Cys Arg Gly Cys Leu Thr Gly

Leu Phe Gly Glu Glu Asp Val Arg Phe Arg Ser Ala Pro Val Tyr Met

Pro Thr Val Val Leu Arg Arg Thr Pro Ala Cys Ala Gly Gly Arg Ser

Val Tyr Thr Glu Ala Tyr Val Thr Ile Pro Val Gly Cys Thr Cys Val 120 125

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Cys Pro Asn Ser Glu Asp Lys Asn Phe Pro Arg Thr Val Met Val Asn

Leu Asn Ile His Asn Arg Asn Thr Asn Thr Asn Pro Lys Arg Ser Ser

Asp Tyr Tyr Asn Arg Ser Thr Ser Pro Trp Asn Leu His Arg Asn Glu

Asp Pro Glu Arg Tyr Pro Ser Val Ile Trp Glu Ala Lys Cys Arg His

Leu Gly Cys Ile Asn Ala Asp Gly Asn Val Asp Tyr His Met Asn Ser 105

Val Pro Ile Gln Gln Glu Ile Leu Val Leu Arg Arg Glu Pro Pro His

Cys Pro Asn Ser Phe Arg Leu Glu Lys Ile Leu Val Ser Val Gly Cys 135

Thr Cys Val Thr Pro Ile Val His His Val Ala 150

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PRT <212>

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Ser Ala Cys Pro Asn Thr Glu Ala Lys Asp Phe Leu Gln Asn Val Lys

Val Asn Leu Lys Val Phe Asn Ser Leu Gly Ala Lys Val Ser Ser Arg

Arg Pro Ser Asp Tyr Leu Asn Arg Ser Thr Ser Pro Trp Thr Leu His

Arg Asn Glu Asp Pro Asp Arg Tyr Pro Ser Val Ile Trp Glu Ala Gln

Cys Arg His Gln Arg Cys Val Asn Ala Glu Gly Lys Leu Asp His His

Met Asn Ser Val Leu Ile Gln Gln Glu Ile Leu Val Leu Lys Arg Glu

Pro Glu Ser Cys Pro Phe Thr Phe Arg Val Glu Lys Met Leu Val Gly

130 135 140

Val Gly Cys Thr Cys Val Ala Ser Ile Val Arg Gln Ala Ala 145 150 155

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Leu Ala Ala Asn Asn Ser Phe Pro Arg Ser Val Met Val Thr Leu Ser 35 40 45

Ile Arg Asn Trp Asn Thr Ser Ser Lys Arg Ala Ser Asp Tyr Tyr Asn 50 55 60

Arg Ser Thr Ser Pro Trp Thr Leu His Arg Asn Glu Asp Gln Asp Arg 65 70 75 80

Tyr Pro Ser Val Ile Trp Glu Ala Lys Cys Arg Tyr Leu Gly Cys Val 85 90 95

Asn Ala Asp Gly Asn Val Asp Tyr His Met Asn Ser Val Pro Ile Gln
100 105 110

Gln Glu Ile Leu Val Val Arg Lys Gly His Gln Pro Cys Pro Asn Ser 115 120 125

Phe Arg Leu Glu Lys Met Leu Val Thr Val Gly Cys Thr Cys Val Thr 130 135 140

Pro Ile Val His Asn Val Asp 145 150

<210> 8

<211> 180

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<213> HOMO SAPIENS

<400> 8

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Leu Gly Leu Gly Gln Pro Arg Ser Pro Lys Ser Lys Arg Lys Gly Gln 20 25 30

Gly Arg Pro Gly Pro Leu Ala Pro Gly Pro His Gln Val Pro Leu Asp 35 40 45

Leu Val Ser Arg Met Lys Pro Tyr Ala Arg Met Glu Glu Tyr Glu Arg

Asn Ile Glu Glu Met Val Ala Gln Leu Arg Asn Ser Ser Glu Leu Ala 65 70 75 80

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Gln Arg Lys Cys Glu Val Asn Leu Gln Leu Trp Met Ser Asn Lys Arg
                85
Ser Leu Ser Pro Trp Gly Tyr Ser Ile Asn His Asp Pro Ser Arg Ile
Pro Val Asp Leu Pro Glu Ala Arg Cys Leu Cys Leu Gly Cys Val Asn
Pro Phe Thr Met Gln Glu Asp Arg Ser Met Val Ser Val Pro Val Phe
    130
Ser Gln Val Pro Val Arg Arg Arg Leu Cys Pro Pro Pro Pro Arg Thr
Gly Pro Cys Arg Gln Arg Ala Val Met Glu Thr Ile Ala Val Gly Cys
                165
Thr Cys Ile Phe
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       5' primer containing a BamHI restriction site followed by
<223>
       several nucleotides of the amino terminal coding
       sequence of mature IL-21 sequence
                                                                        45
gatcgcggat ccgacacgga tgaggaccgc tatccacaga agctg
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       3' primer containing an HindIII restriciton site followed by
        several nucleotides complementary to the 3' end of the
        coding sequence of IL-21 DNA sequence.
 <400> 10
                                                                        41
 cccaagcttt cacactgaac ggggcagcac gcaggtgcag c
 <210> 11
 <211>
        35
 <212>
       DNA
 <213> OLIGONUCLEOTIDE
 <220>
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       (1)..(\overline{3}5)
 <222>
       5' primer containing a BamHI restriction site, a "C" residue
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to preserve the reading frame, and 16 nucleotides of the sequence of the complete IL-21 protein.

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<210> 13 <211> 733 <212> DNA <213> HOMO SAPIENS			
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teteceggae teetgaggte acatgegtgg tggtggaegt aageeaegaa gaeeetgag			
tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca aagccgcgg			
aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg caccaggad			
ggctgaatgg caaggagtac aagtgcaagg tetecaacaa ageeeteeca acceecate	eg 360		
agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac accctgcc	ec 420		
catcccggga tgagctgacc aagaaccagg tcagcctgac ctgcctggtc aaaggctto	et 480		
atccaagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac aactacaa	ga 540		
ccacgcctcc cgtgctggac tccgacggct ccttcttcct ctacagcaag ctcaccgt	gg 600		
acaagagcag gtggcagcag gggaacgtet teteatgete egtgatgeat gaggetet	gc 660		
acaaccacta cacgcagaag agcctctccc tgtctccggg taaatgagtg cgacggcc	gc 720		
gactctagag gat	733		
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Trp Ser Xaa Trp Ser
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       (1)..(86)
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<223> 5' primer containing 14 tandem copies of the GAS-binding
       site, 18bp of complementary sequence to SV40 early
       promotor sequence, and is flanked with an XhoI
       restriction site.
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                                                                       60
                                                                       86
cccgaaatat ctgccatctc aattag
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<221> primer bind
      (1)..(\overline{27})
<222>
<223> 3' primer containing a complementary sequence to SV40 promotor
       and flanked with an Hin dIII site.
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                                                                       27
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<210> 17
<211> 271
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                                                                      120
gcccctaact ccgcccagtt ccgcccattc tccgccccat ggctgactaa tttttttat
                                                                      180
 ttatgcagag gccgaggccg cctcggcctc tgagctattc cagaagtagt gaggaggctt
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                                                                      271
 ttttggaggc ctaggctttt gcaaaaagct t
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      19
                                                                       31
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       primer_bind
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<223> NF-kappaB binding site.
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                                                                        12
ggggactttc cc
<210> 21
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       (1)..(\overline{7}3)
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        binding site, 18bp of complementary sequence to 5' end
        SV40 promotor sequence, flanked by an XhoI restriction site.
 <400> 21
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                                                                        60
                                                                        73
 ccatctcaat tag
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<210> 22

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<220>
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      3' primer containing sequence complementary to the 3' end of the
<223>
       SV40 promotor and flanked by an HindIII restriction site.
<400> 22
                                                                      27
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<211>
<212>
      DNA
<213>
      HOMO SAPIENS
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                                                                      60
caattagtca gcaaccatag tecegeceet aacteegeee ateeegeee taacteegee
                                                                     120
cagttccgcc cattctccgc cccatggctg actaattttt tttatttatg cagaggccga
                                                                     180
                                                                     240
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 <222> (37)...(37)
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170	175	180	
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Thr Pro His Cys Tyr Ser 35	r Ala Glu Glu Leu Pro 40	Leu Gly Gln Ala Pro 45	
Pro His Leu Leu Ala Arg	g Gly Ala Lys Trp Gly 55	Gln Ala Leu Pro Val 60	
Ala Leu Val Ser Ser Leu 65 70	ı Glu Ala Ala Ser His 75	Arg Gly Arg His Glu 80	
Arg Pro Ser Ala Thr Thr 85	r Gln Cys Pro Val Leu 90	Arg Pro Glu Glu Val 95	
Leu Glu Ala Asp Thr His	s Gln Arg Ser Ile Ser 105	Pro Trp Arg Tyr Arg 110	
Val Asp Thr Asp Glu Asp 115	o Arg Tyr Pro Gln Lys 120	Leu Ala Phe Ala Glu 125	

Cys Leu Cys Arg Gly Cys Ile Asp Ala Arg Thr Gly Arg Glu Thr Ala 130 135 140

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Arg Pro Cys Ser Arg Asp Gly Ser Gly Leu Pro Thr Pro Gly Ala Phe
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Leu Ala Ala Gly Val Leu Ser Ala Phe His His Thr Leu Gln Leu Gly
            20
ccg cgt gag cag gcg cgc aac gcg agc tgc ccg gca ggg ggc agg ccc
                                                                       144
Pro Arg Glu Gln Ala Arg Asn Ala Ser Cys Pro Ala Gly Gly Arg Pro
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gec gae ege ege tte egg eeg eee aee aac etg ege age gtg teg eee
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Ala Asp Arg Arg Phe Arg Pro Pro Thr Asn Leu Arg Ser Val Ser Pro
tgg gcc tac aga atc tcc tac gac ccg gcg agg tac ccc agg tac ctg
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Trp Ala Tyr Arg Ile Ser Tyr Asp Pro Ala Arg Tyr Pro Arg Tyr Leu
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cct gaa gcc tac tgc ctg tgc cgg ggc tgc ctg acc ggg ctg ttc ggc
Pro Glu Ala Tyr Cys Leu Cys Arg Gly Cys Leu Thr Gly Leu Phe Gly
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 Val Leu Arg Arg Thr Pro Ala Cys Ala Gly Gly Arg Ser Val Tyr Thr
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Lys Leu Leu	Leu Gly Pro 165	Asn Asp Ala	Pro Ala Gly 170	Pro	